

## Figure 1

An amino acid sequence of human, type I, IMPDH protein

IMPDH = INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1  
514 residues

MADYLISGGT GYVPEDGLTA QQLFASADDL TYNDFLILPG FIDFIADEV  
LTSALTRKIT LKTPLISSPM DTVTEADMAI AMALMGGIGF IHHNCTPEFQ  
ANEVRKVKNF EQGFITDPVV LSPSHTVGDV LEAKMRHGFS GIPITETGTM  
GSKLVGIVTS RDIDFLAEKD HTTLLSEVMT PRIELVVAPA GVTLKEANEI  
LQRSKKGKLP IVNDCDELVA IIARTDLKKN RDYPLASKDS QKQLLCGAAV  
GTREDDKYRL DLLTQAGVDV IVLDSSQGNS VYQIAMVHYI KQKYPHLQVI  
GGNVVTAAQA KNLIDAGVDG LRVGMGCGSI CITQEVMACG RPQGTAVYKV  
AEYARRFGVP IIADGGIQT V GHVVKALALG ASTVMMGSL AATTEAPGEY  
FFSDGVRLKK YRGMGSLDAM EKSSSSQKRY FSEGDKVKIA QGVSGSIQDK  
GSIQKFVPYL IAGIQHGCQD IGARSLSVLR SMMYSGELKF EKRTMSAQIE  
GGVHGLHSYE KRLY

0055918-051004

## Figure 2

An amino acid sequence of human, type II IMPDH protein

IMPDH = INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2  
, 514 residues

The underlined region correlates with the subdomain region

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD  
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ  
ANEVRKVKKY EQGFITDPVV LSPKDRVRDV FEAARHGFC GIPITDTGRM  
GSRLVGIISS RDIDFLKEEE HDCFLEEIMT KREDLVVAPA GITLKEANEI  
LQRSKKGKLP IVNEDDELVA IIARTDLKKN RDYPLASKDA KKQLLCGAAI  
GTTHEDDKYRL DLLAQAGVDV VVLDSSQGNS IFQINMIKYI KDKYPNLQVI  
GGNVVTAAQA KNLIDAGVDA LRVGMGSGSI CITQEVLAGC RPQATAVYKV  
SEYARRFGVP VIADGGIQNV GHIKALALG ASTVMMGSLI AATTEAPGEY  
FFSDGIRLKK YRGMGSLDAM DKHLSSQNRV FSEADKIKVA QGVSGAVQDK  
GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR AMMYSGELKF EKRTSSAQVE  
GGVHSLHSYE KRLF

09853918-051001

FIGURE 3  
The Subdomain of Wild-Type, Human, and Type II  
IMPDH is Replaced with an Oligo-Peptide

Met-1	Tyr-110	Leu-243	Phe-514
	oligo		
	peptide		

## Figure 4

The amino acid sequence of the modified IMPDH-DKT polypeptide 384 residues.

The substitute tri-peptide DKT sequence is highlighted in bold print

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD  
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ  
ANEVRKVKKY **DKT**LLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS  
IFQINMIKYI KDKYPNLQVI GGNVVTAQA KNLIDAGVDA LRVGMGSGSI  
CITQEVLAGG RPQATAVYKV SEYARREGVP VIADGGIQNV GHIKALALG  
ASTVMMGSLA AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY  
FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR  
AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF

095593-051004

## Figure 5

The nucleotide sequence of type II, IMPDH-DKT cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcagctct  
tcaactgctggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga  
ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttccctctcccatg  
gacacagtccacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcaccaccaca  
actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatatgacaagacctgctgtgtgg  
ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctgggtgtggatgta  
gtgggtttggactcttcccagggaattccatcttccagatcaatatgatcaagtacatcaaagacaaat  
accctaattctcaaagtcattggaggcaatgtggtcactgctgccaggccaagaacctcattgatgcagg  
tgtggatgccctgctgggtgggcatgggaagtggctccatctgcattacgcaggaagtgtggcctgtggg  
cgcccccaagcaacagcagtgtagaagggtgcagagtatgcacggcgctttgggtgttccgggtcattgctg  
atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcattgatggg  
ctctctcctgggtgccaccactgaggccctgggtgaatacttcttttccgatgggatccgggttaaagaaa  
tategcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtgaag  
ctgacaaaatcaaagtggcccagggaagtgtctggtgctgtgcaggacaaagggtaaatccacaaatttgt  
cccttacctgattgctggcatccaactcatgccaggacattgggtgccaagagcttgacccaagtcgga  
gccatgatgtactctggggagcttaagtttgagaagagaaacgtcctcagcccagggtggaaggtggcgtcc  
atagcctccattcgtatgagaagcggcttttctga

053918-051001

## Figure 6

The amino acid sequence of the modified IMPDH-SPS  
polypeptide 384 residues.

The substitute tri-peptide SPT sequence is highlighted in  
bold print.

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD  
LTSALT<sup>1</sup>TKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ  
ANEVRKVKKY **SPS**LLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS  
IFQINMIKYI KDKYPNLQVI GGNVVTAQA KNLIDAGVDA LRVGMGSGSI  
CITQEV<sup>2</sup>LACG RPQATAVYKV SEYARREFGVP VIADGGIQNV GHIAKALALG  
ASTVMMGSL<sup>3</sup>L AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY  
FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR  
AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF

095394-051004  
T00T50-BT6586

## FIGURE 7

The nucleotide sequence of type II, IMPDH-SPS cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcagctct  
tcaactgaggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga  
ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagacccactggtttcctctcccatg  
gacacagtcacagaggtgggatggccatagcaatggcgcttacaggcggtattggcttcacccaccaca  
actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatattctccgagcctgctgtgtgg  
ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctgggtgtggatgta  
gtgggttttggactcttcccagggaattccatcttcagatcaatatgatcaagtacatcaaagacaaat  
accctaattctcaaagtcattggaggcaatgtggtcactgctgccaggccaagaacctcattgatgcagg  
tgtggatgccctgcggtgggcatgggaagtggctccatctgcattacgcaggaagtgtggcctgtggg  
cgcccccaagcaacagcagtgtagaaggtgtcagagtatgcacggcgctttgggtgttcgggtcattgctg  
atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcattgatggg  
ctctctcctggctgccaccactgaggccctgggaatacttcttttcgatgggatccggctaaagaaa  
tatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtgaag  
ctgacaaaatcaaagtggcccaggagtgctgtgtgtgcaggacaaagggtcaatccacaaatttgt  
cccttacctgattgctggcatccaacactcatgccaggacattgggtgccaagagcttgacccaagtcgga  
gccatgatgtactctgggagcttaagtttgagaagagaaacgtcctcagcccagggtggaaggtggcgctcc  
atagcctccattcgatgagaagcggctttctga

10985343.054001

## Figure 8

The amino acid sequence of the type II, modified IMPDH-GSG polypeptide

The substitute tri-peptide GSG sequence is highlighted in bold print

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD  
LTSALT<sup>1</sup>KKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ  
ANEVRKVKKY **GSG**LLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS  
IFQINMIKYI KDKYPNLQVI GGNVVTAAQA KNLIDAGVDA LRVGMGSGSI  
CITQEVLAGC RPQATAVYKV SEYARRFGVP VIADGGIQNV GHIKALALG  
ASTVMMGSLI AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY  
FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR  
AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF

09853918-054001



1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--	-----------	--

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcagctct  
tcaactgoggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcaactgcaga  
ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttctctcccatg  
gacacagtacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcattccaccaca  
actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatatggttcgggctgctgtgtgg  
ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgccaggctgggtgtggatgta  
gtggtttggactcttcccagggaattccatcttccagatcaatatgatcaagtacatcaaagacaaat  
acctaagtctccaagtcattggaggcaatgtggtcactgctgccaggccaagaacctcattgatgcagg  
tgtggatgccctgcggtgggcatgggaagtggctccatctgcattacgcaggaagtgtggcctgtggg  
cgcccccaagcaacagcagtgtaacaaggtgtcagagtatgcacggcgctttgggtgttcgggtcattgctg  
atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgatggg  
ctctctcctggctgccaccactgaggccctgggtgaatacttctttccgatgggatcgggtcaagaa  
tatcgcggtattgggtctctctgatgccatggacaagcctcagcagccagacagatatctcagtgaag  
ctgacaaaatcaaagtgccagggcagctgtctgtgtgcaggacaaagggtcaatccacaaatttgt  
cccttaacctgattgtgctggcatccaaagactcatgccaggacattgggtgccaaagacttgacccaagtccga  
gccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccagggtggaaggtggcgctcc  
atagcctccattcgtatgagaagcggcttttctga

## Figure 10

The amino acid sequence of the modified IMPDH-SPT polypeptide 384 residues.

The substitute tri-peptide SPT sequence is highlighted in bold print.

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD  
LTSALT<sup>1</sup>TKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ  
ANEVRKVKKY **SPT**LLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS  
IFQINMIKYI KDKYPNLQVI GGNVVTAQA KNLIDAGVDA LRVGMGSGSI  
CITQEVLAGG RPQATAVYKV SEYARREGVP VIADGGIQNV GHIKALALG  
ASTVMMGSLI AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY  
FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR  
AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF

095918-051001

## Figure 11

The nucleotide sequence of type II, IMPDH-SPT cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcagctct  
tcaactgcgagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga  
ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttccctctccatg  
gacacagtacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcacccaccaca  
actgtacacctgaattccaggccaatgaagttcggaagtgaagaaatattctccgactctgctgtgtgg  
ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctgggtgtggatgta  
gtggttttggactcttcccagggaattccatcttccagatcaatatgatcaagtacatcaaagacaaat  
accctaattctcaagtcattggaggcaatgtggtcactgctgcccaggccaagaacctcattgatgcagg  
tgtggatgccctgcggtgggcatgggaagtggctccatctgcattacgcaggaagtgtgtggcctgtggg  
cgcccccaagcaacagcagtgataaggtgtcagagtatgcacggcgctttgggtgttccggctcattgctg  
atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcattgatggg  
ctctctcctggctgccaccactgaggccctgggaatacttctttccgatgggatccggctaaagaaa  
tatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtgaag  
ctgacaaaatcaaagtggcccaggagtgctgtgtgtgcaggacaaagggccaatccacaaatttgt  
cccttacctgattgctggcatccaacactcatgccaggacattgggtgccaagagcttgacccaagtcgga  
gccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccagggtggaaggtggcgctcc  
atagcctccattcgatgagaagcggcttttctga

100150 8151560

[illegible]

atggccgactacctgattagtgggggcagtcctacgtgccagacgacggactcacagcacagcagctct  
ccaactgcgagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga  
ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactgggtttcctctcccatg  
gacacagtcacagaggctgggtaggcataagcaatggcgcttacaggcggtattggcttcattccaccaca  
actgtacacctgaattccaggccaatgaagtctggaaagtgaagaaatatctccgactcagctgctgtg  
tggggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggtgggtgtggt  
gtagtgggttttgactcttcccagggaattccatcttcagatcaatatgatcaagtacatcaaagaca  
aataccctaatctccaagtcattggaggcaatgtgggtcactgctgccaggccaagaacctcattgatgc  
aggtgtggtatgcctgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgtggcctgt  
gggcggccccaagcaacagcagtgtaacagggtgtcagagtatgcacggcgctttgggtgttcgggtcattg  
ctgatggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcattgat  
gggtctctcctgggtgccaccactgaggccctgggtgaatacttcttttccgatgggatccggctaaag  
aaatatctcggttatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatattcagtg  
aagctgacaaaatcaaagtggcccaggagtgctgtgggtgtgtgcaggacaaagggtaatccacaaatt  
tgtcccttacctgattgtgtggcatccaacactcatgccaggacattgggtgccaagagcttgacccaagtc  
cgagccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccaggtggaaggtggcg  
tccatagcctccattcgatgagaagcggcttttctga

## Figure 13

The amino acid sequence of the modified type II, IMPDH-AGRP polypeptide  
385 residues

The substitute tetra-peptide AGRP sequence is highlighted in bold print.

MADYLISSGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD  
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ  
ANEVRKVKKY **AGRP**LLCGAA IGTHEDDKYR LDLLAQAGVD VVVLDSQGN  
SIFQINMIKY IKDKYPNLQV IGGNVVTAAQ AKNLIDAGVD ALRVGMGSGS  
ICITQEV LAC GRPQATAVYK VSEYARRFGV PVIADGGIQN VGHIAKALAL  
GASTVMMGSL LAATTEAPGE YFFSDGIRLK KYRGMGSLDA MDKHLSSQNR  
YFSEADKIKV AQGVSGAVQD KGSIHKFVPY LIAGIQHSCQ DIGAKSLTQV  
RAMMYSGELK FEKRTSSAQV EGGVHSLHSY EKRLF

0985918 "05400" 8165860

## Figure 14

The nucleotide sequence of type II, IMPDH-AGRP

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcagctct  
tcaaetgcgagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcaactgcaga  
ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttctctcccatg  
gacacagtcacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcacccaccaca  
actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatatgctggctcgccgctgctgtg  
tggggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctgggtgtggat  
gtagtgggttttgactcttcccagggaattccatcttccagatcaatatgatcaagtacatcaaagaca  
aataccctaattctccaagtcattggaggcaatgtggtcactgctgccaggccaagaacctcattgatgc  
aggtgtgagatgacctgcggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgt  
gggcggccccaagcaacagcagtgtaacaaggtgtcagagtatgcacggcgctttgggtgttcgggtcattg  
ctgatggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcattgat  
gggctctctcctggctgccaccactgaggccctgggaatacttcttttccgatgggatccggctaaag  
aaatatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagt  
aagctgacaaaatcaaagtggcccaggagtgctgtggtgctgtgcaggacaaaggtcaatccacaaatt  
tgtcccttacctgattgctggcatccaacactcatgccaggacattgggtgccaagagcttgacccaagtc  
cgagccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccagggtggaaggtggcg  
tccatagcctccattcgtatgagaagcggcttttctga

095948-051004  
T00150-B16E860

## Figure 15

The amino acid sequence of type II, modified IMPDH-NSPL polypeptide

The substitute tri-peptide is highlighted in bold print

MADYLI\$GGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD  
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ  
ANEVRKVKKY **NSPL**LLCGAA IGTHEDDKYR LDLLAQAGVD VVVLDSQGN  
SIFQINMIKY IKDKYPNLQV IGGNVVTAAQ AKNLIDAGVD ALRVGMGSGS  
ICITQEV LAC GRPQATAVYK VSEYARRFGV PVIADGGIQN VGHIAKALAL  
GASTVMMGSL LAATTEAPGE YFFSDGIRLK KYRGMGSLDA MDKHLSSQNR  
YFSEADKIKV AQGVSGAVQD KGSIHKEVPY LIAGIQHSCQ DIGAKSLTQV  
RAMMYSGELK FEKRTSSAQV EGGVHSLHSY EKRLF

095318-0500  
T00T50-816586

## Figure 16

The nucleotide sequence of type II, IMPDH-NSPL cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcagctct  
tcaactgcgagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcaactgcaga  
ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagacccactggtttctctcccatg  
gacacagtcacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcatccaccaca  
actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatataactctccgcttctgctgtg  
tggggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctgggtgtggat  
gtagtggttttggactcttcccagggaattccatcttccagatcaatatgatcaagtacatcaaagaca  
aataccctaattctccaagtcattggaggcaatgtggtcactgctgccaggccaagaacctcattgatgc  
aggtgtggatgcctgcggtgggcatgggaagtggctccatctgcattacgcaggaagtgtggcctgt  
ggcgggccccaagcaacagcagtgtaacagggtgtcagagtatgcacggcgctttgggtgttccggctcattg  
ctgatggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcattg  
gggctctctcctggctgccaccactgaggcccttgggaatacttcttttccgatgggatccggctaaag  
aaatatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagt  
aagctgacaaaatcaaagtggcccaggagtgctgtggtgctgtgcaggacaaagggtcaatccacaaatt  
tgtcccttacctgattgctggcatccaacactcatgccaggacattgggtgccaagagcttgacccaagtc  
cgagccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccagggtggaagggtggcg  
tccatagcctccattcgatgagaagcggttttctga

09853918-051001



Figure 17

The amino acid sequence of the type I modified IMPDH-DKT polypeptide

The substitute tri-peptide DKT is highlighted in bold print

MADYLISGGT GYVPEDGLTA QQLFASADGL TYNDFLILPG FIDFIADDEV  
LTSALTRKIT LKTPLISSPM DTVTEADMAI AMALMGGIGF IHHNCTPEFQ  
ANEVRKVKKF **DKT**LLCGAAV GTREDDKYRL DLLTQAGVDV IVLDSSQGNS  
VYQIAMVHYI KQKYPHLQVI GGNVVTAQA KNLIDAGVDG LRVGMGCGSI  
CITQEVMACG RPQGTAVYKV AEYARRFGVP IIADGGIQT V GHVVKALALG  
ASTVMMGSL AATTEAPGEY FFS DGVR LKK YRGMGSLDAM EKSSSSQKRY  
FSEGDVKIA QGVSGSIQDK GSIQKFVPYL IAGIQHGCQD IGARSLSVLR  
SMMYSGELKF EKRTMSAQIE GGVHGLHSYE KRLY

09653918-051001

Figure 18

A schematic representation of the distance that the substitute oligo-peptides are designed to span in a folded modified IMPDH polypeptide.

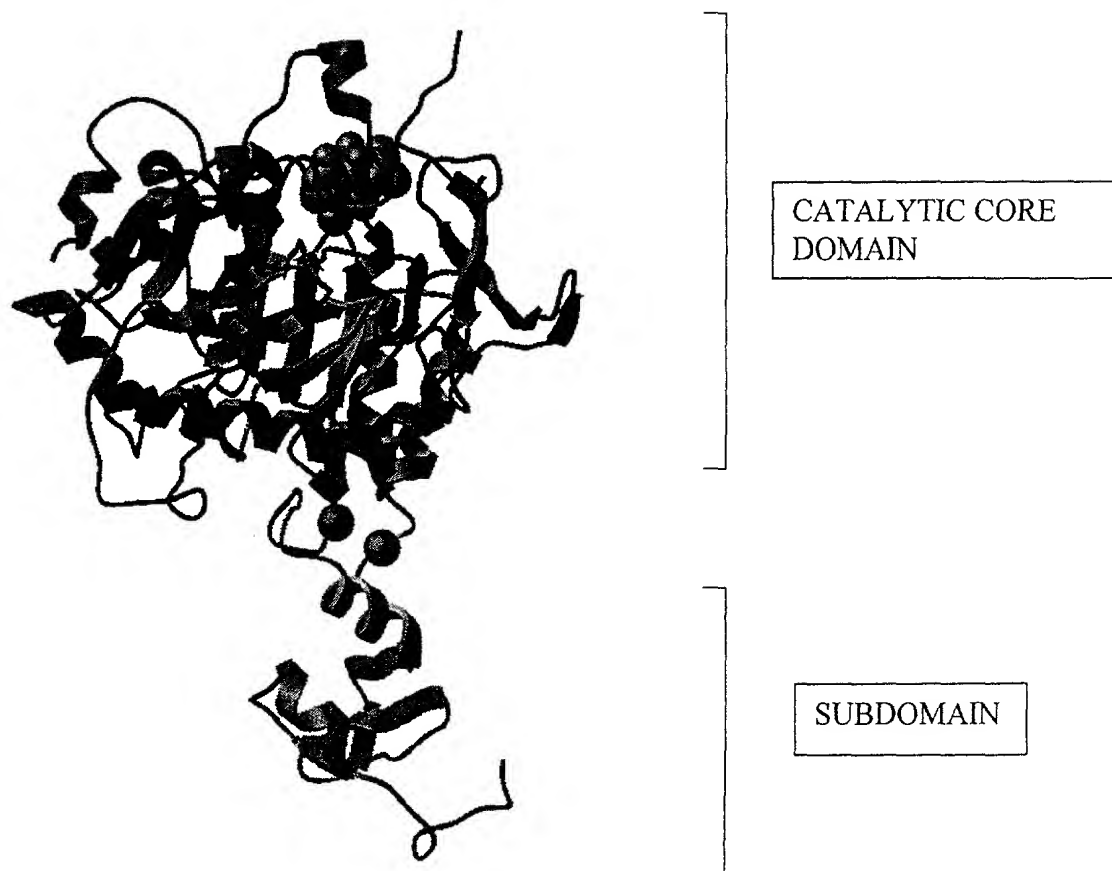


Figure 19

The Rate of NADH Production at 37 °C for Wild-Type IMPDH (type II) and Various Modified IMPDH Multimers.

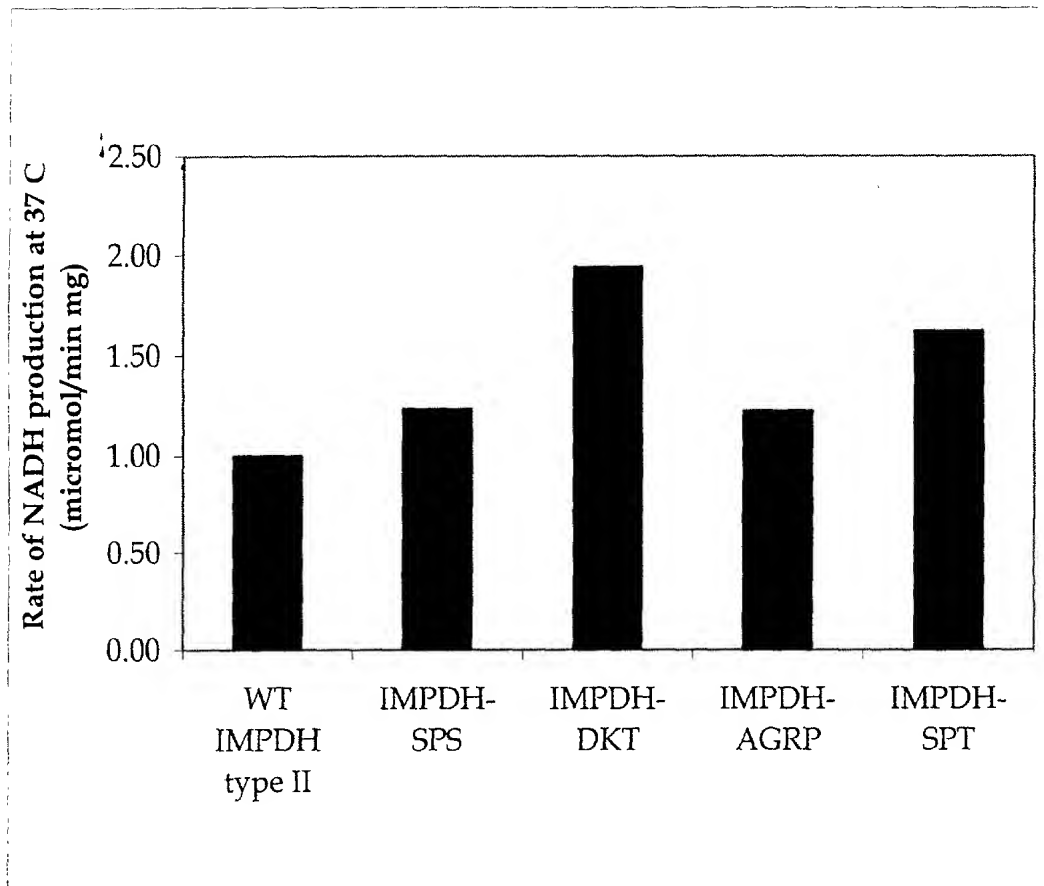
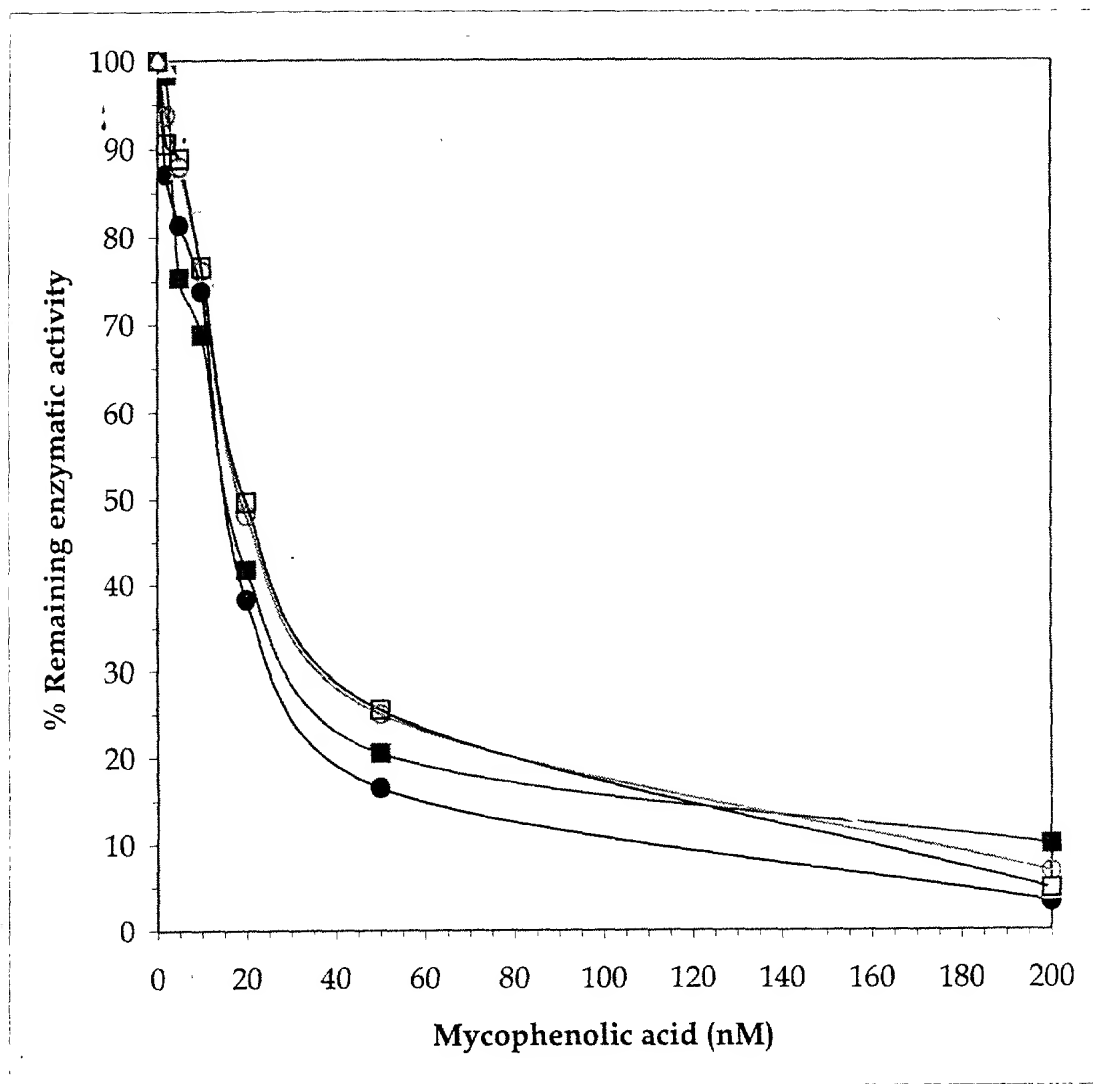


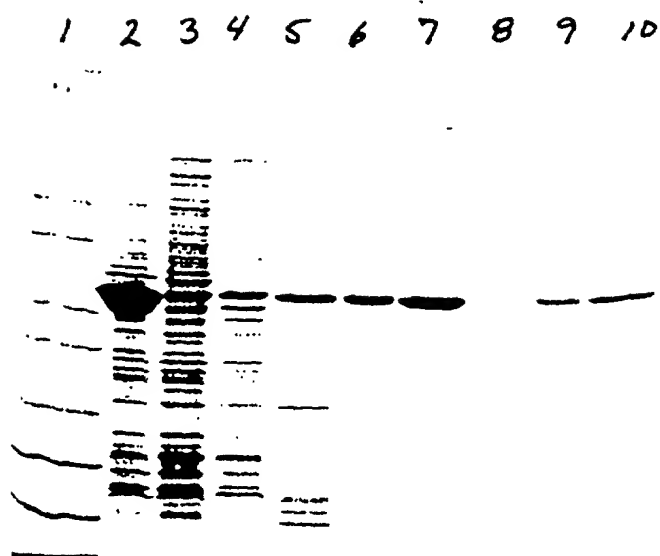
Figure 20

MPA Inhibits the Activity of Various Modified IMPDH Polypeptides.



- wild-type, type II IMPDH
- type II, IMPDH-AGRP
- type II, IMPDH-SPS
- type II, IMPDH-SPT
- ▲ type II, IMPDH-DKT

FIGURE 21



- Lane #
- 1: Novex standards (25  $\mu$ L)
  - 2: Total cell lysate (1  $\mu$ L, 12  $\mu$ g; before ultracentrifugation)
  - 3: Soluble lysate (2.5  $\mu$ L, 10  $\mu$ g; after 100,000  $\times$  g, 1 hr, 4  $^{\circ}$ C)
  - 4: Unbound AE sample (13  $\mu$ L,  $\sim$ 10  $\mu$ g)
  - 5: Blue dye column, frs. #32-70 (25  $\mu$ L, 4.5  $\mu$ g)
  - 6: IMP affinity column, IMP eluted (10  $\mu$ L,  $\sim$ 1.5  $\mu$ g)
  - 7: IMP affinity column, IMP eluted (20  $\mu$ L,  $\sim$ 3.0  $\mu$ g)
  - 8: Unbound protein to IMP column (25  $\mu$ L,  $\sim$ 2.0  $\mu$ g)
  - 9: IMP affinity column (from AE fr. #1-10, 10  $\mu$ L, 1.2  $\mu$ g)
  - 10: IMP affinity column (from AE fr. #1-10, 25  $\mu$ L, 3.0  $\mu$ g)

FIGURE 22

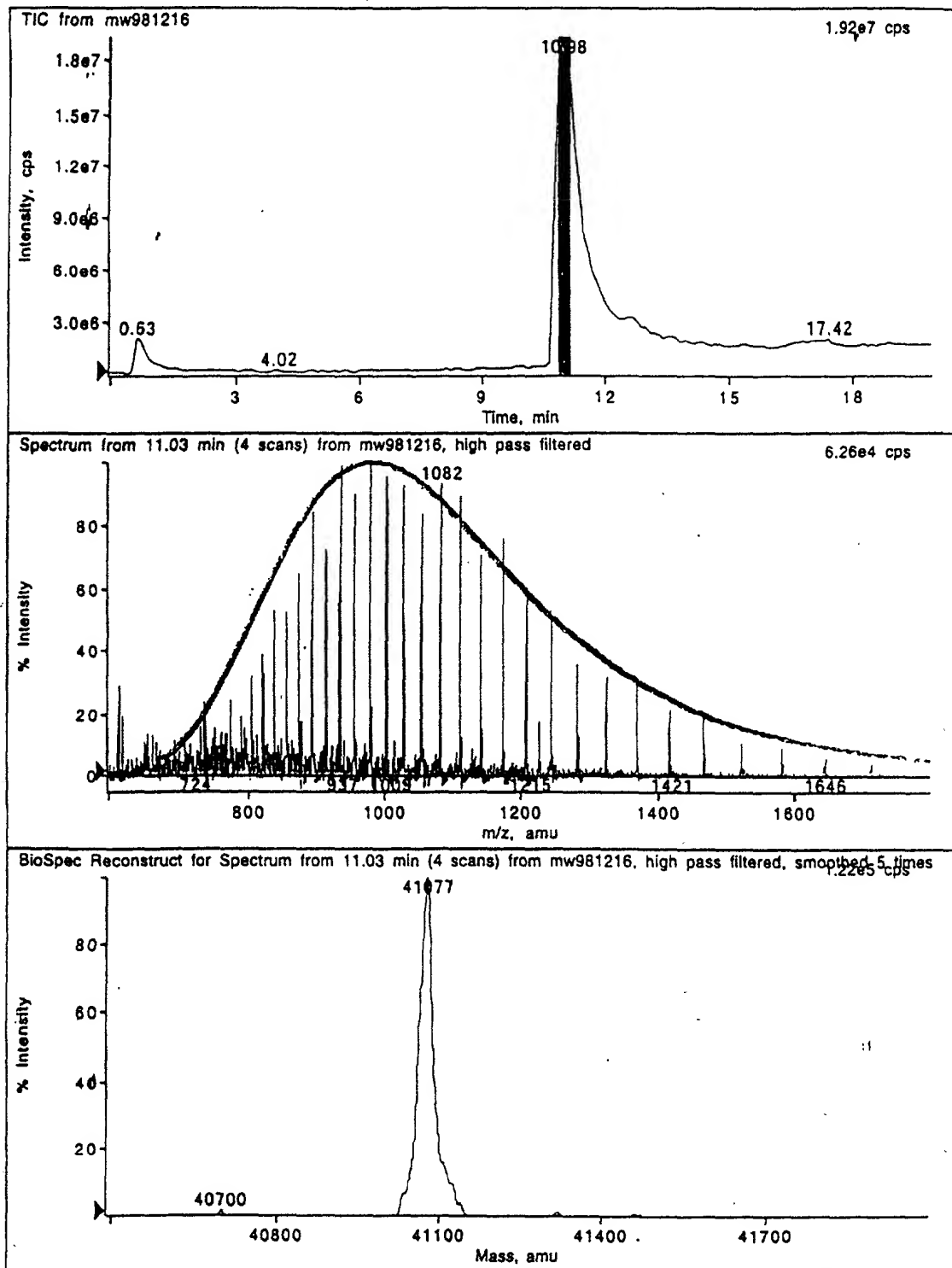
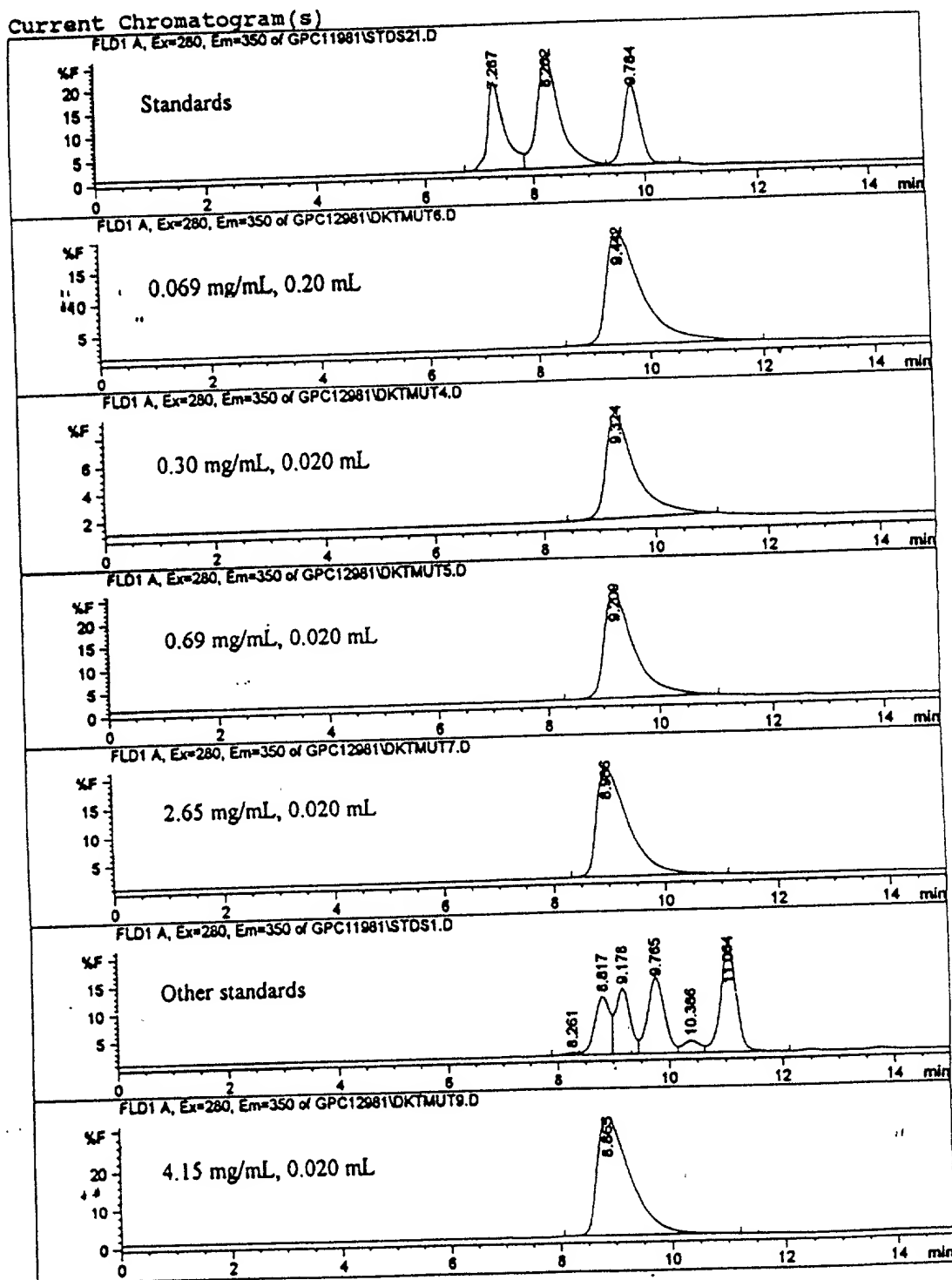


FIGURE 23



FOOT50" 8765860

The nucleotide sequence of type I, IMPDH-DKT

[illegible]